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Inference in Population Genetics Using Forward and Backward,
Discrete and Continuous Time Processes

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Highlights

- Inference of population genetic parameters from a sample of sequences represented as site frequency spectra (SFS), using concepts akin to the forward-backward algorithm of hidden Markov models is described.
- Discrete transition matrices and continuous diffusion models of iterating the population allelic proportion, forward and backward in time, are used for calculating the marginal likelihood of the data for maximum likelihood inference of parameters.
- The method is demonstrated for simulated joint site frequency spectra (i.e., data from two or more populations) under different models of mutation and for different demographic scenarios.

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